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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/816,825A

DATE: 08/06/2003

TIME: 12:19:11

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\08062003\I816825A.raw

4 <110> APPLICANT: BISTRUP, ANNETTE
5 ROSEN, STEVEN D.
6 HEMMERICH, STEFAN
8 <120> TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
11 <130> FILE REFERENCE: UCAL-107CON
13 <140> CURRENT APPLICATION NUMBER: 09/816,825A
14 <141> CURRENT FILING DATE: 2001-03-22
16 <150> PRIOR APPLICATION NUMBER: 09/045,284
17 <151> PRIOR FILING DATE: 1998-03-20
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2032
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <400> SEQUENCE: 1

ENTERED

P.6

```

29 ggctcgaggc caggatgcct ccagttctggg ggaaaatgct tcttcatttg cttctcccag 60
30 cccacctcaa gcagttctccc cacccttga gtctcagcag tgttaaagct gttactttca 120
31 cagcttctctg ggagcgagtg ctttctcaag ccggtcttgc aaggtcttcc acttcagcac 180
32 aatgctactg cctaaaaaaa tgaagctcct gctgtttctg gtttcccaga tggccatctt 240
33 ggctctattc ttccacatgt acagccacaa catcagctcc ctgtctatga aggcacagcc 300
34 cgagcgcatg cacgtgctgg ttctgtcttc ctggcgctct ggctcttctt ttgtggggca 360
35 gctttttggg cagcaccag atgttttcta cctgatggag ccgcctggc acgtgtggat 420
36 gaccttcaag cagagcaccg cctggatgct gcacatggct gtgcgggac tgatacgggc 480
37 cgtcttcttg tgcgacatga gcgtctttga tgccacatg gaacctggc ccggagaca 540
38 gtccagcctc ttccagtggg agaacagccg ggccctgtgt tctgcacctg cctgtgacat 600
39 catcccacaa gatgaaatca tccccgggc tcaactgcag ctctgtgca gtcaacagcc 660
40 ctttgaggtg gtggagaagg cctgccgctc ctacagccac gtggtgctca aggaggtgcg 720
41 cttcttcaac ctgcagtcct tctaccgct gctgaaagac ccctccctca acctgcata 780
42 cgtgcacctg gtccgggacc ccggggcgt gttccgttcc cgagaacgca caaagggaga 840
43 tctcatgatt gacagtcgca ttgtgatggg gcagcatgag cagaaactca agaaggagga 900
44 ccaaccctac tatgtgatgc aggtcatctg ccaaagccag ctggagatct acaagaccat 960
45 ccagtccttg ccaaaggccc tgcaggaaag ctacctgctt gtgcgctatg aggacctggc 1020
46 tgcagccctt gtggcccaga cttcccgaat gtatgaattc gtgggattgg aattcttgcc 1080
47 ccattctcag acctgggtgc ataacatcac ccgaggcaag ggcattgggtg accacgcttt 1140
48 ccacacaaat gccagggatg cccttaatgt ctcccaggct tggcgctggc ctttgcccta 1200
49 tgaaaagggt tctcgacttc agaaagcctg tggcgatgcc atgaatttgc tgggctaccg 1260
50 ccacgtcaga tctgaacaag aacagagaaa cctgttgctg gatcttctgt ctacctggac 1320
51 tgtccctgag caaatccact aagagggttg agaaggcttt gctgccacct ggtgtcagcc 1380
52 tcagtcactt tctctgaatg cttctgagcc ttgcctacat ctctgagcct taactacatg 1440
53 tctgtgggta tcacactgag tgtgagttgt gtccacacgt gctcaagcag aaggactttt 1500
54 gtgtccatgc ttgtgtctag aaaacagact ggggaacctt atgtgagcag cacatcccac 1560
55 cagtgaaca gggatttgct cttcttcttt tcttgatctt cctgtctggg cagacttcag 1620

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```

56 agactttgtg gcctggaggc ctattaagca cgacacagta tcagtggaat tgatccataa 1680
57 acctccctgt ccacatcttg cccaatgggg aatggatctt tcaccaaaga gctcaccagc 1740
58 attttccaca gagatgcaaa ttctgagccc ttggagttcc cagtggattc aaggaaggaa 1800
59 gtgggaacaa gggtggatgc ctacttatga gcttgacctt cacagctatc ggtaatcaga 1860
60 aatatgaaac aaaatctctg caaaaagag caagctotta agttcacagg gtgcctgggc 1920
61 tgcatttgaa tatcacttcc cctctgcatt ttcccatcac atagaagact ttgacctgtg 1980
62 aagctgccat ctgttaatac taaaattccc aaataagaaa aaaaaaaaaa aa 2032

```

64 <210> SEQ ID NO: 2

65 <211> LENGTH: 386

66 <212> TYPE: PRT

67 <213> ORGANISM: Homo sapiens

69 <400> SEQUENCE: 2

```

70 Met Leu Leu Pro Lys Lys Met Lys Leu Leu Leu Phe Leu Val Ser Gln
71 1 5 10 15
72 Met Ala Ile Leu Ala Leu Phe Phe His Met Tyr Ser His Asn Ile Ser
73 20 25 30
74 Ser Leu Ser Met Lys Ala Gln Pro Glu Arg Met His Val Leu Val Leu
75 35 40 45
76 Ser Ser Trp Arg Ser Gly Ser Ser Phe Val Gly Gln Leu Phe Gly Gln
77 50 55 60
78 His Pro Asp Val Phe Tyr Leu Met Glu Pro Ala Trp His Val Trp Met
79 65 70 75 80
80 Thr Phe Lys Gln Ser Thr Ala Trp Met Leu His Met Ala Val Arg Asp
81 85 90 95
82 Leu Ile Arg Ala Val Phe Leu Cys Asp Met Ser Val Phe Asp Ala Tyr
83 100 105 110
84 Met Glu Pro Gly Pro Arg Arg Gln Ser Ser Leu Phe Gln Trp Glu Asn
85 115 120 125
86 Ser Arg Ala Leu Cys Ser Ala Pro Ala Cys Asp Ile Ile Pro Gln Asp
87 130 135 140
88 Glu Ile Ile Pro Arg Ala His Cys Arg Leu Leu Cys Ser Gln Gln Pro
89 145 150 155 160
90 Phe Glu Val Val Glu Lys Ala Cys Arg Ser Tyr Ser His Val Val Leu
91 165 170 175
92 Lys Glu Val Arg Phe Phe Asn Leu Gln Ser Leu Tyr Pro Leu Leu Lys
93 180 185 190
94 Asp Pro Ser Leu Asn Leu His Ile Val His Leu Val Arg Asp Pro Arg
95 195 200 205
96 Ala Val Phe Arg Ser Arg Glu Arg Thr Lys Gly Asp Leu Met Ile Asp
97 210 215 220
98 Ser Arg Ile Val Met Gly Gln His Glu Gln Lys Leu Lys Lys Glu Asp
99 225 230 235 240
100 Gln Pro Tyr Tyr Val Met Gln Val Ile Cys Gln Ser Gln Leu Glu Ile
101 245 250 255
102 Tyr Lys Thr Ile Gln Ser Leu Pro Lys Ala Leu Gln Glu Arg Tyr Leu
103 260 265 270
104 Leu Val Arg Tyr Glu Asp Leu Ala Arg Ala Pro Val Ala Gln Thr Ser
105 275 280 285
106 Arg Met Tyr Glu Phe Val Gly Leu Glu Phe Leu Pro His Leu Gln Thr

```

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```

107      290      295      300
108 Trp Val His Asn Ile Thr Arg Gly Lys Gly Met Gly Asp His Ala Phe
109 305      310      315      320
110 His Thr Asn Ala Arg Asp Ala Leu Asn Val Ser Gln Ala Trp Arg Trp
111      325      330      335
112 Ser Leu Pro Tyr Glu Lys Val Ser Arg Leu Gln Lys Ala Cys Gly Asp
113      340      345      350
114 Ala Met Asn Leu Leu Gly Tyr Arg His Val Arg Ser Glu Gln Glu Gln
115      355      360      365
116 Arg Asn Leu Leu Leu Asp Leu Leu Ser Thr Trp Thr Val Pro Glu Gln
117      370      375      380
118 Ile His
119 385
122 <210> SEQ ID NO: 3
123 <211> LENGTH: 29
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: primer
W--> 130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (9)...(9)
132 <223> OTHER INFORMATION: N = inosine
W--> 134 <221> misc_feature
135 <222> LOCATION: (18)...(18)
136 <223> OTHER INFORMATION: N = inosine
W--> 138 <221> misc_feature
139 <222> LOCATION: (21)...(21)
140 <223> OTHER INFORMATION: N = inosine
W--> 142 <400> 3
W--> 143 twytwyctnt wygarccnct ntggcayst 29
145 <210> SEQ ID NO: 4
146 <211> LENGTH: 29
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: primer
W--> 153 <221> NAME/KEY: misc_feature
154 <222> LOCATION: (3)...(3)
155 <223> OTHER INFORMATION: N = inosine
W--> 157 <221> misc_feature
158 <222> LOCATION: (6)...(6)
159 <223> OTHER INFORMATION: N = inosine
W--> 161 <221> misc_feature
162 <222> LOCATION: (9)...(9)
163 <223> OTHER INFORMATION: N = inosine
W--> 165 <221> misc_feature
166 <222> LOCATION: (12)...(12)
167 <223> OTHER INFORMATION: N = inosine
W--> 169 <221> misc_feature

```

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```

170 <222> LOCATION: (18)...(18)
171 <223> OTHER INFORMATION: N = inosine
W--> 173 <221> misc_feature
174 <222> LOCATION: (21)...(21)
175 <223> OTHER INFORMATION: N = inosine
W--> 177 <221> misc_feature
178 <222> LOCATION: (24)...(24)
179 <223> OTHER INFORMATION: N = inosine
W--> 181 <400> 4
W--> 182 ctnaanctns tncwrcntst nmgnraycc
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 29
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: primer
W--> 192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (6)...(6)
194 <223> OTHER INFORMATION: n = inosine
W--> 196 <221> misc_feature
197 <222> LOCATION: (9)...(9)
198 <223> OTHER INFORMATION: n = inosine
W--> 200 <221> misc_feature
201 <222> LOCATION: (12)...(12)
202 <223> OTHER INFORMATION: n = inosine
W--> 204 <221> misc_feature
205 <222> LOCATION: (18)...(18)
206 <223> OTHER INFORMATION: n = inosine
W--> 208 <221> misc_feature
209 <222> LOCATION: (21)...(21)
210 <223> OTHER INFORMATION: n = inosine
W--> 212 <221> misc_feature
213 <222> LOCATION: (24)...(24)
214 <223> OTHER INFORMATION: n = inosine
W--> 216 <221> misc_feature
217 <222> LOCATION: (27)...(27)
218 <223> OTHER INFORMATION: n = inosine
W--> 220 <400> 5
W--> 221 ggrrtynckna snagywgnas nagnttnag
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 26
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: primer
W--> 231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: (12)...(12)
233 <223> OTHER INFORMATION: n = inosine
W--> 235 <221> misc_feature

```

29

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RAW SEQUENCE LISTING

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TIME: 12:19:11

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\08062003\I816825A.raw

```

236 <222> LOCATION: (15)...(15)
237 <223> OTHER INFORMATION: n = inosine
W--> 239 <221> misc_feature
240 <222> LOCATION: (18)...(18)
241 <223> OTHER INFORMATION: n = inosine
W--> 243 <221> misc_feature
244 <222> LOCATION: (21)...(21)
245 <223> OTHER INFORMATION: n = inosine
W--> 247 <400> 6
W--> 248 agrtcytcrt ancknagnag nakrta 26
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 37
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: primer
258 <400> SEQUENCE: 7
259 aaactcaaga aggaggacca accctactat gtgatgc 37
261 <210> SEQ ID NO: 8
262 <211> LENGTH: 47
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: primer
269 <400> SEQUENCE: 8
270 ataaagcttg tggatttgtt caggacatt ccaggtagac agaagat 47
272 <210> SEQ ID NO: 9
273 <211> LENGTH: 6
274 <212> TYPE: PRT
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: synthetic peptide
280 <400> SEQUENCE: 9
281 Val Arg Tyr Glu Asp Leu
282 1 5
285 <210> SEQ ID NO: 10
286 <211> LENGTH: 29
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: synthetic peptide
W--> 293 <221> NAME/KEY: VARIANT
294 <222> LOCATION: (1)...(1)
295 <223> OTHER INFORMATION: Xaa = T or S
W--> 297 <221> VARIANT
298 <222> LOCATION: 2, 14, 16
299 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 301 <221> VARIANT
302 <222> LOCATION: (9)...(9)

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/06/2003
PATENT APPLICATION: US/09/816,825A TIME: 12:19:12

Input Set : D:\seqlist.txt
Output Set: N:\CRF4\08062003\I816825A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 9,18,21
Seq#:4; N Pos. 3,6,9,12,18,21,24
Seq#:5; N Pos. 6,9,12,18,21,24,27
Seq#:6; N Pos. 12,15,18,21
Seq#:10; Xaa Pos. 1,2,9,11,14,16,17,18,21,23,26,27
Seq#:11; Xaa Pos. 2,4,5,6,7,14,15,16
Seq#:12; Xaa Pos. 2,3,5,6,7,9,10,17,18,19

VERIFICATION SUMMARY

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Input Set : D:\seqlist.txt

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L:130 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:134 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:138 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:142 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:153 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:161 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:192 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:204 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:208 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:212 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:216 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:231 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:235 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:239 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:247 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:293 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:305 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:309 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:317 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:321 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:325 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:329 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:333 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
M:341 Repeated in SeqNo=10
L:348 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:352 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:356 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:360 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:364 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:368 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11

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L:372 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:376 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:380 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:393 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:401 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:405 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:413 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
M:341 Repeated in SeqNo=12